STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 107534

TO: Phillip Gambel **Location: CM1/9E12** **Art Unit: 1644** **Thursday, November 06, 2003** **Case Serial Number: 09761569**	**From: Edward Hart** **Location: Biotech-Chem Library** **CM1-6B02** **Phone: 305-9203** **edward.hart@uspto.gov**

Search Notes

Examiner Gambel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib 107534

From: STIC-ILL
Sent: Tuesday, November 04, 2003 1:06 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/761569 davis amd

Request for you.

-----Original Message-----
From: Gambel, Phillip
Sent: Tuesday, November 04, 2003 1:01 PM
T : STIC-ILL
Subject: 09/761569 davis amd

stic

please provide a sequence and a sequence interference search for

in paper for

ussn 09/761,569 (Davis et al. amd cytokine / stress mmk)

SEQ ID NO: 2

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 11/5/03
Date Completed:_____
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences: 1
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.: 0.0
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:00:01 ; Search time 32 Seconds
(without alignments)
1577.345 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1660	100.0	318	23	ABG32673	Human MKK 3 protei
2	1653	99.6	318	18	AAW06318	Human mitogen-acti
3	1653	99.6	318	20	AAW97668	Human mitogen acti
4	1653	99.6	318	22	AAB31688	A human mitogen-ac
5	1653	99.6	318	22	AAG67438	Amino acid sequenc
6	1653	99.6	318	22	AAG67617	Amino acid sequenc
7	1653	99.6	318	23	ABG32679	Human MKK 3 protei
8	1653	99.6	318	23	AAU80372	Human cellular kin
9	1653	99.6	359	22	ABG12149	Novel human diagno
10	1546	93.1	359	22	ABG23442	Novel human diagno
11	1508	90.8	329	23	ABG79692	Tumour involved ge
12	1359	81.9	334	18	AAW19631	Human mitogen-acti
13	1359	81.9	334	18	AAW06319	Human mitogen-acti
14	1359	81.9	334	20	AAW97669	Human mitogen acti
15	1359	81.9	334	21	AAY57392	Human MAPK kinase
16	1359	81.9	334	22	AAB31689	A human mitogen-ac
17	1359	81.9	334	23	ABG32674	Human mitogen-acti
18	1213	73.1	267	22	ABG07309	Novel human diagno
19	1078	64.9	237	23	ABB57326	Mouse ischaemic co
20	1038	62.5	334	22	ABB60599	Drosophila melanog
21	946	57.0	185	22	AAY72767	Human, MKK3 protei
22	889.5	53.6	399	21	AAY52302	Human K309N mutant
23	888.5	53.5	363	18	AAW06320	Human mitogen-acti
24	888.5	53.5	363	20	AAW97670	Human mitogen acti
25	888.5	53.5	363	22	AAB31690	A human mitogen-ac
26	888.5	53.5	363	23	ABG32675	Human mitogen-acti
27	888.5	53.5	393	18	AAW06321	Human mitogen-acti
28	888.5	53.5	393	20	AAW97671	Human mitogen acti
29	888.5	53.5	393	22	AAB31691	A human mitogen-ac
30	888.5	53.5	393	23	ABG32680	Human MKK 4beta pr
31	888.5	53.5	399	18	AAW06322	Human mitogen-acti
32	888.5	53.5	399	20	AAW97672	Human mitogen acti
33	888.5	53.5	399	21	AAY69970	Human JNKK1 protei
34	888.5	53.5	399	21	AAY52297	Human wild-type pr
35	888.5	53.5	399	22	AAB31692	A human mitogen-ac
36	888.5	53.5	399	23	ABG32677	Human mitogen-acti
37	882.5	53.2	399	21	AAY52298	Human S184L mutant
38	881.5	53.1	399	21	AAY52300	Human R274G mutant
39	877.5	52.9	399	21	AAO20105	399-mer protein se
40	875.5	52.7	399	21	AAO20106	399-mer protein se
41	872.5	52.6	393	23	ABG32676	Human MKK 4beta pr
42	871.5	52.5	399	21	AAO20107	399-mer protein se
43	823	49.6	424	22	ABB64620	Drosophila melanog
44	694	41.8	492	22	ABB58135	Drosophila melanog
45	670	40.4	401	24	ABU03854	Human expressed pr

ALIGNMENTS

RESULT 1
ABG32673
ID ABG32673 standard; Protein; 318 AA.
XX
AC ABG32673;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MKK 3 protein, variation #1.
XX
KW Human; enzyme; mitogen-activated protein kinase kinase; MKK;
KW serine kinase; threonine kinase; tyrosine kinase; phosphorylation;
KW mitogen-activated protein kinase; MAP kinase; p38; MKK-mediated disorder;
KW ischaemic heart disease; kidney failure; oxidative liver damage;
KW respiratory distress syndrome; heat burn; radiation burn; septic shock;
KW rheumatoid arthritis; autoimmune disorder; inflammatory disease;
KW signal transduction; therapeutic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 27
FT /note= "Encoded by AAC"
XX
PN US2002102691-A1.
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2001; 2001US-0761569.
XX
PR 07-APR-1998; 98US-0057009.
PR 08-SEP-1998; 98US-0149879.

```
PR   19-MAY-1995;   95US-0446083.
PR   19-SEP-1995;   95US-0530950.
XX
PA   (UYMA-) UNIV MASSACHUSETTS.
XX
PI   Davis RJ,  Raingeaud J,  Derijard B;
XX
DR   WPI; 2002-682026/73.
DR   N-PSDB; ABS53208.
XX
PT   New human mitogen-activated protein kinase kinase, MKK polypeptide for
PT   identifying reagents that modulate MKK signal transduction pathways, is
PT   capable of phosphorylating human mitogen-activated protein kinase p38
PT   -
XX
PS   Claim 2; Page 15-16; 60pp; English.
XX
CC   The invention discloses substantially pure human mitogen-activated
CC   protein kinase kinase (MKK) polypeptides having serine, threonine and
CC   tyrosine kinase activity and phosphorylating human mitogen-activated
CC   protein (MAP) kinase p38. A MKK specific antibody is useful for measuring
CC   the synthesis of MKK in a biological test sample, which in turn is useful
CC   for identifying a reagent which modulates MKK synthesis. Methods to
CC   measure the activity and expression of MKK are useful for identifying
CC   reagents which modulate, and preferably inhibit, MKK activity. A method
CC   of treating an MKK-mediated disorder in a patient, by administering a
CC   reagent that modulates MKK activity is useful against disorders such as
CC   ischaemic heart disease, kidney failure, oxidative liver damage,
CC   respiratory distress syndrome, heat and radiation burns, septic shock,
CC   rheumatoid arthritis, autoimmune disorders and inflammatory diseases. MKK
CC   polypeptides are useful to produce antibodies that are immunoreactive or
CC   bind epitopes of MKK polypeptides and to screen for reagents that
CC   modulate MKK activity. Reagents that inhibit MKK signal transduction are
CC   useful as therapeutic agents for the treatment of MKK-mediated disorders
CC   and in drug design for elucidation of the specific molecular features
CC   needed to inhibit MKK signal transduction pathways. The sequence
CC   presented is the human MKK3 protein, variation #1.
XX
SQ   Sequence   318 AA;

  Query Match             100.0%;  Score 1660;  DB 23;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-156;
  Matches  318;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 2
AAW06318
ID   AAW06318 standard; Protein; 318 AA.
XX
AC   AAW06318;
XX
DT   07-FEB-1997  (first entry)
XX
DE   Human mitogen-activated protein kinase kinase 3.
XX
KW   Mitogen-activated protein kinase kinase 3; MKK3; MAP;
KW   tyrosine kinase; signal transduction; cytokine; oncoprotein;
KW   stress; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9636642-A1.
XX
PD   21-NOV-1996.
XX
PF   26-JAN-1996;   96WO-US01078.
XX
PR   19-SEP-1995;   95US-0530950.
PR   19-MAY-1995;   95US-0446083.
XX
PA   (DAVI/) DAVIS R J.
PA   (DERI/) DERIJARD B.
PA   (GUPT/) GUPTA S.
PA   (RAIN/) RAINGEAUD J.
XX
PI   Davis RJ,  Derijard B,  Gupta S,  Raingeaud J;
XX
DR   WPI; 1997-012035/01.
DR   N-PSDB; AAT43203.
XX
PT   New mitogen activated protein kinase kinase - useful for treating
PT   ischaemic heart disease, kidney failure etc., also for identifying
PT   modulators for treatment of similar conditions
XX
PS   Claim 2; Fig 4; 104pp; English.
XX
CC   Novel human mitogen activated protein kinase kinase 3 (MKK3)
CC   (AAW06318) has serine, threonine and tyrosine kinase activity, and
CC   mediates a signal transduction pathway that activates human
CC   mitogen-activated protein (MAP) kinase p38.  Its amino acid
CC   sequence was deduced from a cDNA clone (AAT43203) obtd. from a human
CC   foetal brain library.  MKK3 is expressed in all tissues tested, but
CC   partic. in skeletal muscle.  Recombinant MKK3 can be produced in
CC   transformed host cells.  MKKs (AAW06318-22) can be used in the
CC   treatment of MKK-related disorders, e.g. ischaemic heart disease
CC   and kidney failure, to identify modulators of MKK activity, and
CC   to raise antibodies.
XX
SQ   Sequence   318 AA;

  Query Match             99.6%;  Score 1653;  DB 18;  Length 318;
  Best Local Similarity   99.7%;  Pred. No. 8.1e-156;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
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Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

RESULT 3
AAW97668
ID AAW97668 standard; Protein; 318 AA.
XX
AC AAW97668;
XX
DT 10-MAY-1999 (first entry)
XX
DE Human mitogen activated protein kinase kinase MKK3.
XX
KW MKK3; mitogen activated protein kinase kinase; MAP kinase kinase;
KW human; signal transduction; inflammation; psoriasis; AIDS; cancer;
KW apoptosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9902547-A1.
XX
PD 21-JAN-1999.
XX
PF 07-JUL-1998; 98WO-US14101.
XX
PR 07-JUL-1997; 97US-0888429.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Davis RJ, Tournier C, Whitmarsh A;
XX
DR WPI; 1999-120771/10.
DR N-PSDB; AAX07065.
XX
PT New isolated mitogen-activated protein kinase kinase isoforms - used
PT to develop products for treating e.g. inflammatory disorders,
PT oxidative damage, proliferative disorders or autoimmune disorders
XX
PS Example 1; Page 126-127; 168pp; English.
XX
CC This polypeptide comprises human mitogen activated protein (MAP)
CC kinase kinase 3 (MKK3, a 36 kDa protein that phosphorylates p38 but
CC not JNK1 or ERK2. The amino acid sequence was deduced from an
CC isolated human brain cDNA clone (see AAX07065). The human MAP kinase
CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),
CC described in the invention, mediate the transduction of specific
CC signals from the cell surface to the nucleus along specific
CC pathways. They are useful for screening reagents which modulate
CC MKK activity. Such agents can be used to prevent or treat
CC MKK-mediated disorders, e.g. inflammation, oxidative damage or
CC stress-related proliferative disorders, e.g. psoriasis, AIDS,
CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,
CC gastrointestinal system and genito-urinary tract. Agents which
CC inhibit the activity or expression of MKK inhibit cell growth or
CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and
CC polypeptides (see AAW97662-67) are claimed.
XX
SQ Sequence 318 AA;

```
  Query Match            99.6%;  Score 1653;  DB 20;  Length 318;
  Best Local Similarity  99.7%;  Pred. No. 8.1e-156;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

RESULT 4
AAB31688
ID AAB31688 standard; Protein; 318 AA.
XX
AC AAB31688;
XX
DT 30-APR-2001 (first entry)
XX
DE A human mitogen-activated protein kinase kinase MKK3.
XX
KW Mitogen-activated protein kinase kinase; MAP kinase kinase; MKK; MKK3;
KW inflammation; oxidative damage; ischemic heart disease; burn; alcohol;
KW kidney failure; liver damage; oxidative stress; rheumatoid arthritis;
KW respiratory distress syndrome; septic shock; autoimmune disorder;
KW inflammatory disease; proliferative disorder; psoriasis;
KW acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN US6174676-B1.
XX
PD 16-JAN-2001.
XX
PF 08-SEP-1998; 98US-0149879.
XX
PR 07-APR-1998; 98US-0057009.
PR 19-MAY-1995; 95US-0446083.
PR 19-SEP-1995; 95US-0530950.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Davis RJ, Raingeaud J, Derijard B;
XX
DR WPI; 2001-181551/18.
DR N-PSDB; AAF25238.
XX
PT Identifying mitogen-activating protein kinase activity (MKK), synthesis
PT or expression modulators, comprises measuring effect of test reagent on
PT MKK phosphorylation, synthesis or expression after incubation with MKK
PT -
XX
PS Example 1; Fig 4; 59pp; English.
XX
CC The present sequence represents a human mitogen-activated protein (MAP)
CC kinase kinase MKK3. The specification describes a method for identifying
CC a reagent that modulates mitogen-activating MAP kinase kinase (MKK)
CC activity, synthesis or expression. The method comprises incubating MKK
CC with the test reagent and measuring the effect of the test regent on
CC phosphorylation, MKK synthesis or MKK expression. MKK modulating reagents
CC identified by the method of the invention are useful for treating or
CC preventing MKK mediated disorders such as inflammation, oxidative damage,
CC ischemic heart disease, burns due to heat or radiation, kidney failure,
CC liver damage due to oxidative stress or alcohol, respiratory distress
CC syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, and

```
CC   other types of inflammatory diseases and stress-related MKK-mediated
CC   proliferative disorders such as psoriasis, acquired immune deficiency
CC   syndrome, malignancies of various tissues of the body, including
CC   malignancies of the skin, bone marrow, lung, liver, breast etc..
XX
SQ   Sequence   318 AA;

  Query Match             99.6%;  Score 1653;  DB 22;  Length 318;
  Best Local Similarity   99.7%;  Pred. No. 8.1e-156;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 5
AAG67438
ID   AAG67438 standard; Protein; 318 AA.
XX
AC   AAG67438;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Amino acid sequence of a human polypeptide.
XX
KW   Human; protein kinase; protein phosphatase; signal transduction;
KW   intracellular signalling pathway.
XX
OS   Homo sapiens.
XX
PN   WO200109345-A1.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-JP05060.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   18-OCT-1999;   99US-0159590.
PR   11-JAN-2000; 2000JP-0118776.
PR   17-FEB-2000; 2000US-0183322.
PR   02-MAY-2000; 2000JP-0183767.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T,  Funahashi S;
PI   Senoo C,  Nezu J;
XX
DR   WPI; 2001-564736/63.
XX
PT   New genes encoding protein kinase and protein phosphatase, useful for
PT   identifying modulators which can be used to treat human or animal
PT   disorders associated with the expression or function of these enzymes -
XX
PS   Example 4; Page 207-210; 336pp; Japanese.
XX
CC   The specification describes human protein kinase/protein phosphatases.
CC   The polypeptides are expected to participate in signal transduction
CC   in cells. The kinase phosphatases are connected with intracellular
CC   signalling pathways. Antisense oligonucleotides and compounds
CC   identified by screening (agonists or antagonists) can be used to
CC   treat human or animal disorders associated with the expression
CC   or function of the protein. In addition, the polypeptides may be used
CC   as target molecules fir drug development. The present sequence
CC   represents a polypeptide, used in the course of the invention.
XX
SQ   Sequence   318 AA;

  Query Match             99.6%;  Score 1653;  DB 22;  Length 318;
  Best Local Similarity   99.7%;  Pred. No. 8.1e-156;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 6
AAG67617
ID   AAG67617 standard; Protein; 318 AA.
XX
AC   AAG67617;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Amino acid sequence of a human protein.
XX
KW   Human; protein kinase; protein phosphatase; signal transduction.
XX
OS   Homo sapiens.
XX
PN   WO200109316-A1.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-JP05061.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   18-OCT-1999;   99US-0159590.
PR   11-JAN-2000; 2000JP-0118776.
PR   17-FEB-2000; 2000US-0183322.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
```

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI; 2001-570286/64.
XX
PT New genes encoding proteins with protein kinase/protein phosphatase
PT activity, useful in the diagnosis and treatment of diseases -
XX
PS Example 4; Page 106-108; 233pp; Japanese.
XX
CC The specification describes human protein kinase/protein phosphatases.
CC It is expected that the protein kinase/protein phosphatase gene
CC participates in signal transduction in cells. The protein
CC kinase/protein phosphatase polypeptides and polynucleotides are
CC useful for developing diagnostics and treatment agents for human
CC and animal diseases. The protein kinase/protein phosphatase polypeptides
CC are useful as target molecules in designing novel drugs. The protein
CC kinase/protein phosphatase polynucleotides are useful as a source of
CC probes and primers, which may be used to isolate homologous sequences.
CC The present sequence represents a human protein, which is used in the
CC course of the invention.
XX
SQ Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 22; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

RESULT 7
ABG32679
ID ABG32679 standard; Protein; 318 AA.
XX
AC ABG32679;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MKK 3 protein, variation #2.
XX
KW Human; enzyme; mitogen-activated protein kinase kinase; MKK;
KW serine kinase; threonine kinase; tyrosine kinase; phosphorylation;
KW mitogen-activated protein kinase; MAP kinase; p38; MKK-mediated disorder;
KW ischaemic heart disease; kidney failure; oxidative liver damage;
KW respiratory distress syndrome; heat burn; radiation burn; septic shock;
KW rheumatoid arthritis; autoimmune disorder; inflammatory disease;
KW signal transduction; therapeutic.
XX
OS Homo sapiens.
XX
PN US2002102691-A1.
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2001; 2001US-0761569.
XX
PR 07-APR-1998; 98US-0057009.
PR 08-SEP-1998; 98US-0149879.
PR 19-MAY-1995; 95US-0446083.
PR 19-SEP-1995; 95US-0530950.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Davis RJ, Raingeaud J, Derijard B;
XX
DR WPI; 2002-682026/73.
DR N-PSDB; ABS53208.
XX
PT New human mitogen-activated protein kinase kinase, MKK polypeptide for
PT identifying reagents that modulate MKK signal transduction pathways, is
PT capable of phosphorylating human mitogen-activated protein kinase p38
PT -
XX
PS Disclosure; Fig 1; 60pp; English.
XX
CC The invention discloses substantially pure human mitogen-activated
CC protein kinase kinase (MKK) polypeptides having serine, threonine and
CC tyrosine kinase activity and phosphorylating human mitogen-activated
CC protein (MAP) kinase p38. A MKK specific antibody is useful for measuring
CC the synthesis of MKK in a biological test sample, which in turn is useful
CC for identifying a reagent which modulates MKK synthesis. Methods to
CC measure the activity and expression of MKK are useful for identifying
CC reagents which modulate, and preferably inhibit, MKK activity. A method
CC of treating an MKK-mediated disorder in a patient, by administering a
CC reagent that modulates MKK activity is useful against disorders such as
CC ischaemic heart disease, kidney failure, oxidative liver damage,
CC respiratory distress syndrome, heat and radiation burns, septic shock,
CC rheumatoid arthritis, autoimmune disorders and inflammatory diseases. MKK
CC polypeptides are useful to produce antibodies that are immunoreactive or
CC bind epitopes of MKK polypeptides and to screen for reagents that
CC modulate MKK activity. Reagents that inhibit MKK signal transduction are
CC useful as therapeutic agents for the treatment of MKK-mediated disorders
CC and in drug design for elucidation of the specific molecular features
CC needed to inhibit MKK signal transduction pathways. The sequence
CC presented is the human MKK3 protein, variation #2.
XX
SQ Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 23; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
```

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Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

RESULT 8
AAU80372
ID AAU80372 standard; Protein; 318 AA.
XX
AC AAU80372;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human cellular kinase MKK3 protein.
XX
KW Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;
KW RIP; Nck-Interacting kinase; MKK3; SRPK-2.
XX
OS Homo sapiens.
XX
PN EP1201765-A2.
XX
PD 02-MAY-2002.
XX
PF 15-OCT-2001; 2001EP-0124604.
XX
PR 16-OCT-2000; 2000US-240750P.
XX
PA (AXXI-) AXXIMA PHARM AG.
XX
PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
XX
DR WPI; 2002-373930/41.
DR N-PSDB; ABK51172.
XX
PT Identifying agents for treatment or prevention of cytomegalovirus
PT infection, comprises contacting test compound with cellular kinase and
PT detecting change in cellular kinase activity -
XX
PS Disclosure; Page 38-39; 49pp; English.
XX
CC The present invention relates to a new method for identifying compounds
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC related diseases. The method of the invention comprises contacting a
CC test compound with at least one of the cellular kinases RICK, RIP,
CC Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in
CC kinase activity. The method of the invention can be used to treat and/or
CC prevent CMV infections and related diseases. Oligonucleotides that can
CC detect the specified kinases can also be used for diagnosis of infection.
CC The present amino acid sequence represents the human cellular kinase MKK3
CC protein of the invention, as described above.
XX
SQ Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 23; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

RESULT 9
ABG12149
ID ABG12149 standard; Protein; 359 AA.
XX
AC ABG12149;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12140.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS76336.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 42508; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 359 AA;

```
  Query Match             99.6%;  Score 1653;  DB 22;  Length 359;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-156;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         42 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 101

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 161

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 221

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 281

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 341

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        342 TKKTDIAAFVKKILGEDS 359


RESULT 10
ABG23442
ID   ABG23442 standard; Protein; 359 AA.
XX
AC   ABG23442;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #23433.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87629.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 53801; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   359 AA;

  Query Match             93.1%;  Score 1546;  DB 22;  Length 359;
  Best Local Similarity   93.7%;  Pred. No. 4.3e-145;
  Matches  298;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         42 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 101

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 161

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 221

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              |||||||||||||::||||    | :||:||:|| :||| |||||||||||| ||||||
Db        222 GISGYLVDSVAKTINAGCKVKHGHESLNPDLNRKGCDVKSHVWSLGITMIEMAFLRFPYE 281

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Db        282 SWGTPFQQLKQVVEHPSPQLPAGRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 341

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||:||||||||:||||||
Db        342 TKETDIAAFVKEILGEDS 359


RESULT 11
ABG79692
ID   ABG79692 standard; Protein; 329 AA.
XX
AC   ABG79692;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Tumour involved gene (TIG) splice variant protein, NV-23.
XX
KW   Human; splice variant; tumour-involved gene; TIG;
KW   pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW   endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002086384-A1.
XX
PD   04-JUL-2002.
XX
PF   13-MAR-2001; 2001US-0805020.
XX
PR   14-MAR-2000; 2000IL-0135402.
PR   16-MAY-2000; 2000IL-0136154.
XX
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```
PA   (LEVI/) LEVINE Z.
PA   (DAVI/) DAVID A.
PA   (ROMA/) ROMANO C.
PA   (BERN/) BERNSTEIN J.
XX
PI   Levine Z,  David A,  Romano C,  Bernstein J;
XX
DR   WPI; 2002-635679/68.
DR   N-PSDB; ABS65222.
XX
PT   Novel nucleic acid sequence, which is an alternative splicing variant
PT   of tumor involved genes, useful for detecting cancer, predisposition to
PT   cancer, for evaluating cancer state and in gene therapy for treating
PT   cancer -
XX
PS   Claim 4; Page 91; 180pp; English.
XX
CC   The invention discloses isolated human nucleic acid alternative splicing
CC   variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC   polypeptides are useful for determining the level of a nucleic acid or
CC   polypeptide in a biological sample, for detecting a variant nucleic acid
CC   or polypeptide sequence in a biological sample, for determining the level
CC   of variant nucleic acid or polypeptide sequences in a biological sample
CC   and for determining the ratio between the level of variant sequence in a
CC   first biological sample and the level of the original sequence from which
CC   the variant has been varied by alternative splicing in a second
CC   biological sample and for raising antibodies. A pharmaceutical
CC   composition comprising a carrier and the nucleic acid, is useful for
CC   treating diseases (e.g. cancer) that can be ameliorated or cured by
CC   increasing or decreasing the level of the encoded protein. The nucleic
CC   acids are also useful for diagnostic purposes, especially for detecting
CC   cancer or a predisposition to cancer, for evaluating the state or
CC   aggressiveness of cancer disease, in basic research, for understanding
CC   the physiological function of the original TIG, in targeting or
CC   developing pharmaceuticals, for distinguishing various stages in the life
CC   cycle of the same type of cells which may be helpful for the development
CC   of pharmaceuticals for various cancer stages in which cell cycle is
CC   non-normal, for determining mutations in tumour-involved genes and in
CC   gene therapy. The polypeptides are useful for identifying compounds
CC   capable of binding to the variant product and modulating its activity
CC   and for modulating endothelial differentiation and proliferation, as well
CC   as to modulate apoptosis either ex vivo or in vivo. The sequences
CC   presented in ABG796700-ABG79705 are the new variants (NV) 1-36 proteins
CC   of the TIGs disclosed.
XX
SQ   Sequence   329 AA;

  Query Match             90.8%;  Score 1508;  DB 23;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-141;
  Matches  289;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         30 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 89

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 149

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 209

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 269

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELM 291
              |||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        270 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELI 320


RESULT 12
AAW19631
ID   AAW19631 standard; Protein; 334 AA.
XX
AC   AAW19631;
XX
DT   01-SEP-1997  (first entry)
XX
DE   Human mitogen-activated protein kinase kinase MEK6.
XX
KW   MEK-6; mitogen-activated protein kinase kinase; MAPKK; p38;
KW   signal transduction; cell proliferation; osteoarthritis; ischaemia;
KW   reperfusion injury; trauma; cancer; autoimmune disease;
KW   rheumatoid arthritis; multiple sclerosis; psoriasis;
KW   inflammatory bowel disease; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO9722704-A1.
XX
PD   26-JUN-1997.
XX
PF   20-DEC-1996;   96WO-US20233.
XX
PR   20-DEC-1995;   95US-0576240.
XX
PA   (SIGN-) SIGNAL PHARM INC.
XX
PI   Stein B,  Yang MXH;
XX
DR   WPI; 1997-341695/31.
DR   N-PSDB; AAT68716.
XX
PT   Mitogen-activated protein kinase kinase and corresponding DNA -
PT   phosphorylates p38 cascade members, used in the treatment of
PT   immunological-related cell proliferative diseases
XX
PS   Claim 1; Page 31-33; 67pp; English.
XX
CC   Human mitogen-activated protein kinase kinase MEK6 (AAW19631) is a
CC   protein capable of modulating the activity of the mitogen-activated
CC   protein kinase p38 (esp. p38-2).  Its amino acid sequence was
CC   deduced from a cDNA clone (AAT68716) obtd. from a MOLT-4 cDNA
CC   library.  MEK6 is 88% identical to its closest homologue MKK3,
CC   and all relevant kinase subdomains are conserved.  MEK6
CC   polypeptides can be produced in transformed or transfected host
CC   cells.  MEK6 and its variants, antibodies raised against MEK6, and
CC   MEK6 nucleic acids can be used to modulate (stimulate or inhibit)
CC   phosphorylation of p38 by MEK6 for use in the treatment of diseases
CC   associated with the p38 cascade e.g. immunological-related cell
CC   proliferative diseases and autoimmune diseases, and also to detect
CC   MEK6 kinase activity and identify proteins that interact with MEK6.
XX
SQ   Sequence   334 AA;

  Query Match             81.9%;  Score 1359;  DB 18;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-126;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | |||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:|||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||:||||:|||||||||:|||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262
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Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| |||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 13
AAW06319
ID   AAW06319 standard; Protein; 334 AA.
XX
AC   AAW06319;
XX
DT   07-FEB-1997  (first entry)
XX
DE   Human mitogen-activated protein kinase kinase 6.
XX
KW   Mitogen-activated protein kinase kinase 6; MKK6; MAP;
KW   tyrosine kinase; signal transduction; cytokine; oncoprotein;
KW   stress; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9636642-A1.
XX
PD   21-NOV-1996.
XX
PF   26-JAN-1996;   96WO-US01078.
XX
PR   19-SEP-1995;   95US-0530950.
PR   19-MAY-1995;   95US-0446083.
XX
PA   (DAVI/) DAVIS R J.
PA   (DERI/) DERIJARD B.
PA   (GUPT/) GUPTA S.
PA   (RAIN/) RAINGEAUD J.
XX
PI   Davis RJ,  Derijard B,  Gupta S,  Raingeaud J;
XX
DR   WPI; 1997-012035/01.
DR   N-PSDB; AAT43204.
XX
PT   New mitogen activated protein kinase kinase - useful for treating
PT   ischaemic heart disease, kidney failure etc., also for identifying
PT   modulators for treatment of similar conditions
XX
PS   Claim 6; Fig 5; 104pp; English.
XX
CC   Novel human mitogen activated protein kinase kinase 6 (MKK6)
CC   (AAW06319) has serine, threonine and tyrosine kinase activity, and
CC   mediates a signal transduction pathway that activates human
CC   mitogen-activated protein (MAP) kinase p38.  Its amino acid
CC   sequence was deduced from a cDNA clone (AAT43204) obtd. from a human
CC   skeletal muscle library.  Recombinant MKK6 can be produced in
CC   transformed host cells.  MKKs (AAW06318-22) are useful in the
CC   treatment of MKK-related disorders, e.g. ischaemic heart disease
CC   and kidney failure, for identifying modulators of MKK activity,
CC   and for raising antibodies.
XX
SQ   Sequence   334 AA;

  Query Match             81.9%;  Score 1359;  DB 18;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-126;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:|| || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:||||||:|||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| |||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 14
AAW97669
ID   AAW97669 standard; Protein; 334 AA.
XX
AC   AAW97669;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Human mitogen activated protein kinase kinase MKK6.
XX
KW   MKK6; mitogen activated protein kinase kinase; MAP kinase kinase;
KW   human; signal transduction; inflammation; psoriasis; AIDS; cancer;
KW   apoptosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9902547-A1.
XX
PD   21-JAN-1999.
XX
PF   07-JUL-1998;   98WO-US14101.
XX
PR   07-JUL-1997;   97US-0888429.
XX
PA   (UYMA-) UNIV MASSACHUSETTS.
XX
PI   Davis RJ,  Tournier C,  Whitmarsh A;
XX
DR   WPI; 1999-120771/10.
DR   N-PSDB; AAX07066.
XX
PT   New isolated mitogen-activated protein kinase kinase isoforms - used
PT   to develop products for treating e.g. inflammatory disorders,
PT   oxidative damage, proliferative disorders or autoimmune disorders
XX
PS   Disclosure; Page 129; 168pp; English.
XX
CC   This polypeptide comprises human mitogen activated protein (MAP)
CC   kinase kinase 6 (MKK6).  The amino acid sequence was deduced from an
CC   isolated human skeletal muscle cDNA clone (see AAX07066) and shows
CC   high homology to human MKK3 (see AAW97668).  The human MAP kinase
CC   kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),
CC   described in the invention, mediate the transduction of specific
CC   signals from the cell surface to the nucleus along specific
CC   pathways.  They are useful for screening reagents which modulate
CC   MKK activity.  Such agents can be used to prevent or treat
CC   MKK-mediated disorders, e.g. inflammation, oxidative damage or
CC   stress-related proliferative disorders, e.g. psoriasis, AIDS,
CC   malignancies of e.g. the skin, bone marrow, lung, liver, breast,
CC   gastrointestinal system and genito-urinary tract.  Agents which
CC   inhibit the activity or expression of MKK inhibit cell growth or
CC   cause apoptosis.  MKK7 polynucleotides (see AAX07059-64) and
CC   polypeptides (see AAW97662-67) are claimed.
```

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XX
SQ   Sequence   334 AA;

  Query Match           81.9%;  Score 1359;  DB 20;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-126;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              |||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 15
AAY57392
ID   AAY57392 standard; Protein; 334 AA.
XX
AC   AAY57392;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human MAPK kinase 6 polypeptide.
XX
KW   Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense;
KW   sandwich assay; human.
XX
OS   Homo sapiens.
XX
PN   US6033910-A.
XX
PD   07-MAR-2000.
XX
PF   19-JUL-1999;   99US-0357073.
XX
PR   19-JUL-1999;   99US-0357073.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-269479/23.
DR   N-PSDB; AAZ98598.
XX
PT   Novel antisense oligonucleotides used for inhibition of
PT   Mitogen-activated protein kinase kinase 6 expression  -
XX
PS   Example 13; Columns 45-50; 33pp; English.
XX
CC   The invention provides antisense oligonucleotides which are targeted to a
CC   nucleic acid encoding a mitogen-activated protein kinase (MAPK) kinase 6.
CC   The antisense oligonucleotides are used to inhibit MAPK kinase 6
CC   expression, and so are used to treat diseases mediated by MAPK kinase 6
CC   expression. They may also be used to detect MAPK kinase 6, e.g. in
CC   sandwich assays. The present sequence represents the human MAPK kinase 6.
```

```
XX
SQ   Sequence   334 AA;

  Query Match           81.9%;  Score 1359;  DB 21;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-126;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
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Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              |||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


Search completed: November  5, 2003, 20:03:48
Job time : 33 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:03:52 ; Search time 22 Seconds
(without alignments)
611.584 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1660	100.0	318	1	US-08-530-950-2	Sequence 2, Appli
2	1660	100.0	318	3	US-09-149-879-2	Sequence 2, Appli
3	1660	100.0	318	4	US-09-057-009-2	Sequence 2, Appli
4	1653	99.6	318	3	US-08-888-429A-2	Sequence 2, Appli
5	1644	99.0	318	1	US-08-446-083-2	Sequence 2, Appli
6	1359	81.9	334	1	US-08-530-950-4	Sequence 4, Appli
7	1359	81.9	334	3	US-08-576-240-2	Sequence 2, Appli
8	1359	81.9	334	3	US-08-888-429A-4	Sequence 4, Appli
9	1359	81.9	334	3	US-09-149-879-4	Sequence 4, Appli
10	1359	81.9	334	4	US-09-057-009-4	Sequence 4, Appli
11	946	57.0	185	4	US-09-384-162-11	Sequence 11, Appl
12	888.5	53.5	363	1	US-08-530-950-6	Sequence 6, Appli
13	888.5	53.5	363	3	US-08-888-429A-6	Sequence 6, Appli
14	888.5	53.5	363	3	US-09-149-879-6	Sequence 6, Appli
15	888.5	53.5	363	4	US-09-057-009-6	Sequence 6, Appli
16	888.5	53.5	393	3	US-08-888-429A-8	Sequence 8, Appli
17	888.5	53.5	399	1	US-08-530-950-10	Sequence 10, Appl
18	888.5	53.5	399	2	US-08-874-186-92	Sequence 92, Appl
19	888.5	53.5	399	3	US-08-888-429A-10	Sequence 10, Appl
20	888.5	53.5	399	3	US-09-149-879-10	Sequence 10, Appl
21	888.5	53.5	399	4	US-09-057-009-10	Sequence 10, Appl
22	872.5	52.6	393	1	US-08-530-950-8	Sequence 8, Appli
23	872.5	52.6	393	3	US-09-149-879-8	Sequence 8, Appli
24	872.5	52.6	393	4	US-09-057-009-8	Sequence 8, Appli
25	697	42.0	393	3	US-08-888-429A-21	Sequence 21, Appl
26	697	42.0	487	4	US-09-206-166-6	Sequence 6, Appli
27	670	40.4	419	4	US-09-206-166-2	Sequence 2, Appli
28	670	40.4	435	4	US-09-446-754-2	Sequence 2, Appli
29	664	40.0	389	3	US-08-888-429A-20	Sequence 20, Appl
30	664	40.0	419	3	US-08-888-429A-28	Sequence 28, Appl
31	664	40.0	419	4	US-09-446-754-6	Sequence 6, Appli
32	664	40.0	419	4	US-09-206-166-5	Sequence 5, Appli
33	664	40.0	468	4	US-09-446-754-4	Sequence 4, Appli
34	660.5	39.8	453	3	US-08-888-429A-32	Sequence 32, Appl
35	660	39.8	346	3	US-08-888-429A-18	Sequence 18, Appl
36	657.5	39.6	380	3	US-08-888-429A-30	Sequence 30, Appl
37	657	39.6	468	4	US-09-446-754-10	Sequence 10, Appl
38	586	35.3	367	3	US-08-888-429A-13	Sequence 13, Appl
39	573	34.5	393	1	US-08-423-399B-33	Sequence 33, Appl
40	573	34.5	393	1	US-08-530-950-11	Sequence 11, Appl
41	573	34.5	393	3	US-08-888-429A-11	Sequence 11, Appl
42	573	34.5	393	3	US-09-149-879-11	Sequence 11, Appl
43	573	34.5	393	4	US-09-057-009-11	Sequence 11, Appl
44	570.5	34.4	668	1	US-08-530-950-13	Sequence 13, Appl
45	570.5	34.4	668	3	US-09-149-879-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-530-950-2
; Sequence 2, Application US/08530950
; Patent No. 5736381
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Raingeaud, Joel
; APPLICANT: Gupta, Shashi
; APPLICANT: Derijard, Benoit
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
; TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,950
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07917/010001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-08-530-950-2

Query Match 100.0%; Score 1660; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.7e-158;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

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Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
                 ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 2
US-09-149-879-2
; Sequence 2, Application US/09149879
; Patent No. 6174676
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/149,879
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
US-09-149-879-2

  Query Match           100.0%;  Score 1660;  DB 3;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-158;
  Matches  318;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
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Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 3
US-09-057-009-2
; Sequence 2, Application US/09057009
; Patent No. 6541605
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,009
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  No. 6541605 Relevant
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;      TOPOLOGY:  linear
US-09-057-009-2

  Query Match             100.0%;  Score 1660;  DB 4;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-158;
  Matches  318;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
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Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
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Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 4
US-08-888-429A-2
; Sequence 2, Application US/08888429A
; Patent No. 6136596
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Whitmarsh, Alan
;    APPLICANT:  Tournier, Cathy
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;    TITLE OF INVENTION:  ACTIVATED HUMAN PROTEIN KINASE KINASES
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,429A
;      FILING DATE:  07-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:  19-SEP-1995
;      APPLICATION NUMBER:  08/446,083
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, Peter J.
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  299354
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-888-429A-2

  Query Match             99.6%;  Score 1653;  DB 3;  Length 318;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-157;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
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Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
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Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 5
US-08-446-083-2
; Sequence 2, Application US/08446083
; Patent No. 5804427
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-,STRESS-,AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,083
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  04020/066001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
```

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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  both
;    MOLECULE TYPE:  protein
US-08-446-083-2

  Query Match            99.0%;  Score 1644;  DB 1;  Length 318;
  Best Local Similarity  99.4%;  Pred. No. 1.5e-156;
  Matches  316;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRESPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318


RESULT 6
US-08-530-950-4
; Sequence 4, Application US/08530950
; Patent No. 5736381
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/530,950
;      FILING DATE:  19-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
US-08-530-950-4

  Query Match            81.9%;  Score 1359;  DB 1;  Length 334;
  Best Local Similarity  82.4%;  Pred. No. 5.5e-128;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              |||||||||||||||||||:|||||| :|||||||||||||||||||||||||||:|:
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:||||||:|||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              |||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 7
US-08-576-240-2
; Sequence 2, Application US/08576240
; Patent No. 6074862
;  GENERAL INFORMATION:
;    APPLICANT:  Stein, Bernd
;    APPLICANT:  Yang, Maria
;    TITLE OF INVENTION:  MITOGEN-ACTIVATED PROTEIN KINASE KINASE
;    TITLE OF INVENTION:  MEK6 AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/576,240
;      FILING DATE:  20-DEC-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  860098.403
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  2:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-576-240-2

  Query Match             81.9%;  Score 1359;  DB 3;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 5.5e-128;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              |||||||||||||||||||:|||||| :|||||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:|||||:|||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 8
US-08-888-429A-4
; Sequence 4, Application US/08888429A
; Patent No. 6136596
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Whitmarsh, Alan
;    APPLICANT:  Tournier, Cathy
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;    TITLE OF INVENTION:  ACTIVATED HUMAN PROTEIN KINASE KINASES
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,429A
;      FILING DATE:  07-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:  19-SEP-1995
;      APPLICATION NUMBER:  08/446,083
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, Peter J.
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  299354
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-888-429A-4

  Query Match             81.9%;  Score 1359;  DB 3;  Length 334;
  Best Local Similarity   82.4%;  Pred. No. 5.5e-128;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              |||||||||||||||||||:|||||| :|||||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:|||||:|||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 9
US-09-149-879-4
; Sequence 4, Application US/09149879
; Patent No. 6174676
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/149,879
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
```

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;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
US-09-149-879-4

  Query Match            81.9%;  Score 1359;  DB 3;  Length 334;
  Best Local Similarity  82.4%;  Pred. No. 5.5e-128;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:||||||:||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 10
US-09-057-009-4
; Sequence 4, Application US/09057009
; Patent No. 6541605
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,009
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  No. 6541605 Relevant
;      TOPOLOGY:  linear
US-09-057-009-4

  Query Match            81.9%;  Score 1359;  DB 4;  Length 334;
  Best Local Similarity  82.4%;  Pred. No. 5.5e-128;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  |||||||:||||||:||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 11
US-09-384-162-11
; Sequence 11, Application US/09384162
; Patent No. 6376747
; GENERAL INFORMATION:
;  APPLICANT: Xing, Ti
;  APPLICANT: Malik, Kamal
;  APPLICANT: Martin-Heller, Teresa
;  APPLICANT: Miki L., Brian
;  TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
;  FILE REFERENCE: O8-884280US
;  CURRENT APPLICATION NUMBER: US/09/384,162
;  CURRENT FILING DATE: 1999-08-27
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-384-162-11

  Query Match            57.0%;  Score 946;  DB 4;  Length 185;
  Best Local Similarity  88.5%;  Pred. No. 5.5e-87;
  Matches  185;  Conservative    0;  Mismatches    0;  Indels   24;  Gaps    1;
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Qy          35 LVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYT 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 LVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYT 60

Qy          95 VTFYGALFREGDVWICMELMDTSLDKFYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSK 154
               ||||||||||||||||||||||||||||||||||
Db          61 VTFYGALFREGDVWICMELMDTSLDKFYRKVLDKNM---------------------- 96

Qy         155 LSVIHRDVKPSNVLINKEGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQK 214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          97 LSVIHRDVKPSNVLINKEGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQK 156

Qy         215 GYNVKSDVWSLGITMIEMAILRFPYESWG 243
               ||||||||||||||||||||||||||||
Db         157 GYNVKSDVWSLGITMIEMAILRFPYESWG 185


RESULT 12
US-08-530-950-6
; Sequence 6, Application US/08530950
; Patent No. 5736381
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/530,950
;      FILING DATE:  19-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
US-08-530-950-6

  Query Match             53.5%;  Score 888.5;  DB 1;  Length 363;
  Best Local Similarity   52.6%;  Pred. No. 8.2e-81;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy           7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
               ||||  :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db          27 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 86

Qy          56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
                 || ||||||||:||: :|||:||||||: ||: || | | ||||||||||| |||||||
Db          87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy         116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
               || ||||:    |||    |||:|||:|| :: |:|| ||   | :||||:||||:|:::
Db         147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy         173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
               |::|:||||||| ||||:||| ||||:||||||||:|  :::||:|:|||||||||: |:
Db         205 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 264

Qy         233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
               |  ||||  | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db         265 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 324

Qy         290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
               |::|||  ::: :  ::| :| ||| :
Db         325 LLKHPFILMYEERAVEVACYVCKILDQ 351


RESULT 13
US-08-888-429A-6
; Sequence 6, Application US/08888429A
; Patent No. 6136596
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Whitmarsh, Alan
;    APPLICANT:  Tournier, Cathy
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;    TITLE OF INVENTION:  ACTIVATED HUMAN PROTEIN KINASE KINASES
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,429A
;      FILING DATE:  07-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:  19-SEP-1995
;      APPLICATION NUMBER:  08/446,083
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, Peter J.
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  299354
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-888-429A-6

  Query Match             53.5%;  Score 888.5;  DB 3;  Length 363;
  Best Local Similarity   52.6%;  Pred. No. 8.2e-81;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy           7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
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Db          27 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 86
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Qy          56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
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Db          87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy         116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
               || ||||:    |||    |||:|||:| :: |:|| ||   | :||||:||||:|:::
Db         147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy         173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
               |::|:|||||| ||||:||| ||||:||||||:|  :::||:|:|||||||: |:
Db         205 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 264

Qy         233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
               |  |||| | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db         265 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEERFSPSFINFVNLCLTKDESKRPKYKE 324

Qy         290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
               |::|||  ::: :  ::| :| ||| :
Db         325 LLKHPFILMYEERAVEVACYVCKILDQ 351


RESULT 14
US-09-149-879-6
; Sequence 6, Application US/09149879
; Patent No. 6174676
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/149,879
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
US-09-149-879-6

  Query Match             53.5%;  Score 888.5;  DB 3;  Length 363;
  Best Local Similarity   52.6%;  Pred. No. 8.2e-81;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy           7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
               ||||  :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db          27 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 86

Qy          56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || |||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db          87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy         116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
               || ||||:    |||    |||:|||:| :: |:|| ||   | :||||:||||:|:::
Db         147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy         173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
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Qy         233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
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Qy         290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
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Db         325 LLKHPFILMYEERAVEVACYVCKILDQ 351


RESULT 15
US-09-057-009-6
; Sequence 6, Application US/09057009
; Patent No. 6541605
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Roger J.
;    APPLICANT:  Raingeaud, Joel
;    APPLICANT:  Gupta, Shashi
;    APPLICANT:  Derijard, Benoit
;    TITLE OF INVENTION:  CYTOKINE-, STRESS-, AND
;    TITLE OF INVENTION:  ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;    TITLE OF INVENTION:  KINASES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,009
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/530,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/010001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  No. 6541605 Relevant
;      TOPOLOGY:  linear
US-09-057-009-6
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Query Match 53.5%; Score 888.5; DB 4; Length 363;
Best Local Similarity 52.6%; Pred. No. 8.2e-81;
Matches 172; Conservative 60; Mismatches 76; Indels 19; Gaps 5;

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Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
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Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || ||||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db         87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|:::
Db        147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
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Db        205 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 264

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db        265 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEERFSPSFINFVNLCLTKDESKRPKYKE 324

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
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Db        325 LLKHPFILMYEERAVEVACYVCKILDQ 351
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Search completed: November 5, 2003, 20:09:31
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:04:52 ; Search time 42 Seconds
(without alignments)
1300.387 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1660	100.0	318	10	US-09-761-569-2	Sequence 2, Appli
2	1653	99.6	318	11	US-09-981-397A-20	Sequence 20, Appl
3	1653	99.6	318	15	US-10-059-585-36	Sequence 36, Appl
4	1653	99.6	318	16	US-10-137-953-2	Sequence 2, Appli
5	1359	81.9	333	12	US-10-406-730-2	Sequence 2, Appli
6	1359	81.9	334	10	US-09-761-569-4	Sequence 4, Appli
7	1359	81.9	334	16	US-10-137-953-4	Sequence 4, Appli
8	888.5	53.5	363	10	US-09-761-569-6	Sequence 6, Appli
9	888.5	53.5	363	16	US-10-137-953-6	Sequence 6, Appli
10	888.5	53.5	393	16	US-10-137-953-8	Sequence 8, Appli
11	888.5	53.5	399	10	US-09-761-569-10	Sequence 10, Appl
12	888.5	53.5	399	15	US-10-288-222A-8	Sequence 8, Appli
13	888.5	53.5	399	16	US-10-137-953-10	Sequence 10, Appl
14	872.5	52.6	393	10	US-09-761-569-8	Sequence 8, Appli
15	697	42.0	393	16	US-10-137-953-21	Sequence 21, Appl
16	668	40.2	419	12	US-10-204-041-6	Sequence 6, Appli
17	664	40.0	389	16	US-10-137-953-20	Sequence 20, Appl
18	664	40.0	419	16	US-10-137-953-28	Sequence 28, Appl
19	660.5	39.8	453	16	US-10-137-953-32	Sequence 32, Appl
20	660	39.8	346	16	US-10-137-953-18	Sequence 18, Appl
21	657.5	39.6	380	16	US-10-137-953-30	Sequence 30, Appl
22	586	35.3	367	16	US-10-137-953-13	Sequence 13, Appl
23	573	34.5	389	10	US-09-755-665-36	Sequence 36, Appl
24	573	34.5	393	10	US-09-761-569-11	Sequence 11, Appl
25	573	34.5	393	11	US-09-918-873-4	Sequence 4, Appli
26	573	34.5	393	16	US-10-137-953-11	Sequence 11, Appl
27	572.5	34.5	600	15	US-10-128-714-3202	Sequence 3202, Ap
28	572.5	34.5	656	15	US-10-128-714-8202	Sequence 8202, Ap
29	570.5	34.4	668	10	US-09-761-569-13	Sequence 13, Appl
30	570.5	34.4	668	10	US-09-801-368-238	Sequence 238, App
31	570.5	34.4	668	15	US-10-081-119-20	Sequence 20, Appl
32	566	34.1	400	10	US-09-761-569-12	Sequence 12, Appl
33	565.5	34.1	545	12	US-10-032-585-7762	Sequence 7762, Ap
34	565	34.0	395	10	US-09-755-665-34	Sequence 34, Appl
35	565	34.0	400	16	US-10-137-953-12	Sequence 12, Appl
36	564	34.0	400	12	US-09-769-970-17	Sequence 17, Appl
37	560	33.7	400	12	US-09-769-970-3	Sequence 3, Appli
38	550.5	33.2	359	12	US-10-159-971A-4	Sequence 4, Appli
39	550.5	33.2	405	16	US-10-137-953-22	Sequence 22, Appl
40	550.5	33.2	448	12	US-10-159-971A-1	Sequence 1, Appli
41	539	32.5	364	10	US-09-755-665-64	Sequence 64, Appl
42	531	32.0	392	10	US-09-755-665-35	Sequence 35, Appl
43	531	32.0	394	10	US-09-755-665-33	Sequence 33, Appl
44	519	31.3	380	10	US-09-755-665-8	Sequence 8, Appli
45	495	29.8	369	10	US-09-755-665-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
US-09-761-569-2
; Sequence 2, Application US/09761569
; Patent No. US20020102691A1
;  GENERAL INFORMATION:
;       APPLICANT: Davis, Roger J.
;                  Raingeaud, Joel
;                  Gupta, Shashi
;                  Derijard, Benoit
;       TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
;                           ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;                           KINASES
;       NUMBER OF SEQUENCES: 16
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson P.C.
;            STREET: 225 Franklin Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110-2804
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/761,569
;            FILING DATE: 16-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/057,009
;            FILING DATE: 1998-04-07
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fasse, J. Peter
;            REGISTRATION NUMBER: 32,983
;            REFERENCE/DOCKET NUMBER: 07917/010001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617/542-5070
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;             TELEFAX: 617/542-8906
;             TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 318 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: No. US20020102691A1 Relevant
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-761-569-2

  Query Match            100.0%;  Score 1660;  DB 10;  Length 318;
  Best Local Similarity  100.0%;  Pred. No. 9.3e-149;
  Matches  318;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
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Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
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RESULT 2
US-09-981-397A-20
; Sequence 20, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
;  APPLICANT: Axxima Pharmaceuticals AG
;  APPLICANT:  Schubart, Daniel
;  APPLICANT:  Habenberger, Peter
;  APPLICANT:  Stein-Gerlach, Matthias
;  APPLICANT:  Bevec, Dorian
;  TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
;  TITLE OF INVENTION:  Inhibition
;  FILE REFERENCE: AXM-004.1 US
;  CURRENT APPLICATION NUMBER: US/09/981,397A
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: 60/240,750
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 318
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-981-397A-20

  Query Match            99.6%;  Score 1653;  DB 11;  Length 318;
  Best Local Similarity  99.7%;  Pred. No. 4.3e-148;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
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RESULT 3
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; Sequence 36, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
;  APPLICANT: Ota, Toshio
;  APPLICANT:  Isogai, Takao
;  APPLICANT:  Nishikawa, Tetsuo
;  APPLICANT:  Hayashi, Koji
;  APPLICANT:  Otsuka, Kaoru
;  APPLICANT:  Yamamoto, Jun-ichi
;  APPLICANT:  Ishii, Shizuko
;  APPLICANT:  Sugiyama, Tomoyasu
;  APPLICANT:  Wakamatsu, Ai
;  APPLICANT:  Nagai, Keiichi
;  APPLICANT:  Otsuki, Tetsuji
;  APPLICANT:  Funahashi, Shin-Ichi
;  APPLICANT:  Senoo, Chiaki
;  APPLICANT:  Nezu, Jun-Ichi
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
;  TITLE OF INVENTION:  KINASE/PROTEIN PHOSPHATASE
;  FILE REFERENCE: 06501-098001
;  CURRENT APPLICATION NUMBER: US/10/059,585
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/JP00/05060
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/183,322
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: US 60/159,590
;  PRIOR FILING DATE: 1999-10-18
;  PRIOR APPLICATION NUMBER: JP 2000-118776
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: JP 2000-183767
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: JP 11-248036
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 318
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-059-585-36

  Query Match            99.6%;  Score 1653;  DB 15;  Length 318;
  Best Local Similarity  99.7%;  Pred. No. 4.3e-148;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
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Qy          61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy         121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy         181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy         241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy         301 TKKTDIAAFVKKILGEDS 318
               ||||||||||||||||||
Db         301 TKKTDIAAFVKKILGEDS 318
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RESULT 4
US-10-137-953-2
; Sequence 2, Application US/10137953
; Publication No. US20030129606A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; Whitmarsh, Alan
; Tournier, Cathy
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
; ACTIVATED HUMAN PROTEIN KINASE KINASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/137,953
; FILING DATE: 03-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,429
; FILING DATE: 07-JUL-1997
; APPLICATION NUMBER: 08/530,950
; FILING DATE: 19-SEP-1995
; APPLICATION NUMBER: 08/446,083
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07917/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 299354
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-137-953-2

Query Match 99.6%; Score 1653; DB 16; Length 318;
Best Local Similarity 99.7%; Pred. No. 4.3e-148;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy           1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy          61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy         121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy         181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy         241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy         301 TKKTDIAAFVKKILGEDS 318
               ||||||||||||||||||
Db         301 TKKTDIAAFVKKILGEDS 318
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RESULT 5
US-10-406-730-2
; Sequence 2, Application US/10406730
; Publication No. US20030175928A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Bernd
; APPLICANT: Yang, Maria X. H.
; TITLE OF INVENTION: MITOGEN-ACTIVATED PROTEIN KINASE KINASE
; TITLE OF INVENTION: MEK6 AND METHODS OF USE THEREFOR
; FILE REFERENCE: 860098.403C1
; CURRENT APPLICATION NUMBER: US/10/406,730
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/593,288
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/576,240
; PRIOR FILING DATE: 1995-12-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo sapien
US-10-406-730-2

Query Match 81.9%; Score 1359; DB 12; Length 333;
Best Local Similarity 82.4%; Pred. No. 3e-120;
Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

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Qy           5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
               |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:|| || |||||
Db          22 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 81

Qy          65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
               ||||||||||||||||||:|||||| :|||||||||||||||||||||||||||||::
Db          82 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 141

Qy         125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
               |:||  ||||||||:||||||:|||||||||||||||||||||  | ||||||||||
Db         142 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 201

Qy         185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
               |||||||||:|||||||||||||||||||:||||:|||||||||:|||||||:||||
Db         202 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 261

Qy         245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
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                  ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        262 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 321

Qy        305 DIAAFVKKILGE 316
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Db        322 DVASFVKLILGD 333


RESULT 6
US-09-761-569-4
; Sequence 4, Application US/09761569
; Patent No. US20020102691A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Raingeaud, Joel
;                   Gupta, Shashi
;                   Derijard, Benoit
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
;                            ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;                            KINASES
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/761,569
;             FILING DATE: 16-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/057,009
;             FILING DATE: 1998-04-07
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, J. Peter
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/010001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 334 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: No. US20020102691A1 Relevant
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-761-569-4

  Query Match            81.9%;  Score 1359;  DB 10;  Length 334;
  Best Local Similarity  82.4%;  Pred. No. 3e-120;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:|| || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              |||||||||||||||||:|||||| :|||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              ||||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
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Db        323 DVASFVKLILGD 334


RESULT 7
US-10-137-953-4
; Sequence 4, Application US/10137953
; Publication No. US20030129606A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Whitmarsh, Alan
;                   Tournier, Cathy
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;                            ACTIVATED HUMAN PROTEIN KINASE KINASES
;        NUMBER OF SEQUENCES: 34
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/137,953
;             FILING DATE: 03-May-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/888,429
;             FILING DATE: 07-JUL-1997
;             APPLICATION NUMBER: 08/530,950
;             FILING DATE: 19-SEP-1995
;             APPLICATION NUMBER: 08/446,083
;             FILING DATE: 19-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, Peter J.
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/053001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 299354
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 334 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-137-953-4

  Query Match            81.9%;  Score 1359;  DB 16;  Length 334;
  Best Local Similarity  82.4%;  Pred. No. 3e-120;
  Matches  257;  Conservative   30;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:|||| | ||||||||||||:|| || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
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                 |||||||||||||||||||:|||||| :|||||||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              |||||||||||||||||:|| ||||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334


RESULT 8
US-09-761-569-6
; Sequence 6, Application US/09761569
; Patent No. US20020102691A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Raingeaud, Joel
;                   Gupta, Shashi
;                   Derijard, Benoit
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
;                            ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;                            KINASES
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/761,569
;             FILING DATE: 16-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/057,009
;             FILING DATE: 1998-04-07
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, J. Peter
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/010001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 363 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: No. US20020102691A1 Relevant
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-761-569-6

  Query Match           53.5%;  Score 888.5;  DB 10;  Length 363;
  Best Local Similarity  52.6%;  Pred. No. 1.1e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              ||||  :|          ::|   : |  :: ::  |:||  : |:||||||  | |: |
Db         27 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 86

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || ||||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db         87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|:::
Db        147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||||| ||||:||| ||||:||||||||:|  :::||:|:|||||||||: |:
Db        205 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 264

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  |||| | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db        265 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 324

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        325 LLKHPFILMYEERAVEVACYVCKILDQ 351


RESULT 9
US-10-137-953-6
; Sequence 6, Application US/10137953
; Publication No. US20030129606A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Whitmarsh, Alan
;                   Tournier, Cathy
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;                            ACTIVATED HUMAN PROTEIN KINASE KINASES
;        NUMBER OF SEQUENCES: 34
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/137,953
;             FILING DATE: 03-May-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/888,429
;             FILING DATE: 07-JUL-1997
;             APPLICATION NUMBER: 08/530,950
;             FILING DATE: 19-SEP-1995
;             APPLICATION NUMBER: 08/446,083
;             FILING DATE: 19-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, Peter J.
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/053001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 299354
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 363 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
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;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-137-953-6

  Query Match            53.5%;  Score 888.5;  DB 16;  Length 363;
  Best Local Similarity  52.6%;  Pred. No. 1.1e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              |||| :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         27 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 86

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || |||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db         87 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 146

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||   | :||||:||||:|:::
Db        147 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 204

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||| ||||:||| |||||||||||:|  :::||:|:|||||||||: |:
Db        205 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 264

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||      ||| |::|   || |: ::|  | |
Db        265 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 324

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        325 LLKHPFILMYEERAVEVACYVCKILDQ 351


RESULT 10
US-10-137-953-8
; Sequence 8, Application US/10137953
; Publication No. US20030129606A1
;   GENERAL INFORMATION:
;       APPLICANT: Davis, Roger J.
;                  Whitmarsh, Alan
;                  Tournier, Cathy
;       TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;                           ACTIVATED HUMAN PROTEIN KINASE KINASES
;       NUMBER OF SEQUENCES: 34
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson P.C.
;            STREET: 225 Franklin Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110-2804
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/137,953
;            FILING DATE: 03-May-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/888,429
;            FILING DATE: 07-JUL-1997
;            APPLICATION NUMBER: 08/530,950
;            FILING DATE: 19-SEP-1995
;            APPLICATION NUMBER: 08/446,083
;            FILING DATE: 19-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fasse, Peter J.
;            REGISTRATION NUMBER: 32,983
;            REFERENCE/DOCKET NUMBER: 07917/053001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617/542-5070
;            TELEFAX: 617/542-8906
;            TELEX: 299354

;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 393 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-137-953-8

  Query Match            53.5%;  Score 888.5;  DB 16;  Length 393;
  Best Local Similarity  52.6%;  Pred. No. 1.2e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              |||| :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         57 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 116

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || |||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db        117 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 176

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||   | :||||:||||:|:::
Db        177 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 234

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||| ||||:||| |||||||||||:|  :::||:|:|||||||||: |:
Db        235 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 294

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||      ||| |::|   || |: ::|  | |
Db        295 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 354

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        355 LLKHPFILMYEERAVEVACYVCKILDQ 381


RESULT 11
US-09-761-569-10
; Sequence 10, Application US/09761569
; Patent No. US20020102691A1
;   GENERAL INFORMATION:
;       APPLICANT: Davis, Roger J.
;                  Raingeaud, Joel
;                  Gupta, Shashi
;                  Derijard, Benoit
;       TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
;                           ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;                           KINASES
;       NUMBER OF SEQUENCES: 16
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson P.C.
;            STREET: 225 Franklin Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110-2804
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/761,569
;            FILING DATE: 16-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/057,009
;            FILING DATE: 1998-04-07
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fasse, J. Peter
```

```
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/010001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 399 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: No. US20020102691A1 Relevant
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-761-569-10

  Query Match             53.5%;  Score 888.5;  DB 10;  Length 399;
  Best Local Similarity   52.6%;  Pred. No. 1.2e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              |||| :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         63 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 122

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || ||||||||:||: :|||:|||||||: ||: || | | |||||||||| |||||||
Db        123 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 182

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|:::
Db        183 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 240

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||||| ||||:||| ||||:||||||||:|  :::||:|:|:||||||||: |:
Db        241 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 300

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db        301 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 360

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        361 LLKHPFILMYEERAVEVACYVCKILDQ 387


RESULT 12
US-10-288-222A-8
; Sequence 8, Application US/10288222A
; Publication No. US20030119742A1
; GENERAL INFORMATION:
;  APPLICANT: Logan, Thomas Joseph
;  APPLICANT:  Galvin, Katherine
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: Methods and Compositions to treat
;  TITLE OF INVENTION:  Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414,
;  TITLE OF INVENTION:  10183, 10550, 12680, 17921, 32248, 60489 OR 93804
;  FILE REFERENCE: MPI2001-286P1R(M)
;  CURRENT APPLICATION NUMBER: US/10/288,222A
;  CURRENT FILING DATE:  2002-11-05
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-288-222A-8

  Query Match             53.5%;  Score 888.5;  DB 15;  Length 399;
  Best Local Similarity   52.6%;  Pred. No. 1.2e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              |||| :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         63 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 122

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || ||||||||:||: :|||:|||||||: ||: || | | |||||||||| |||||||
Db        123 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 182

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|:::
Db        183 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 240

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||||| ||||:||| ||||:||||||||:|  :::||:|:|:||||||||: |:
Db        241 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 300

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||       ||| |::|   || |: ::|  | |
Db        301 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 360

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        361 LLKHPFILMYEERAVEVACYVCKILDQ 387


RESULT 13
US-10-137-953-10
; Sequence 10, Application US/10137953
; Publication No. US20030129606A1
;  GENERAL INFORMATION:
;       APPLICANT: Davis, Roger J.
;                  Whitmarsh, Alan
;                  Tournier, Cathy
;       TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;                           ACTIVATED HUMAN PROTEIN KINASE KINASES
;       NUMBER OF SEQUENCES: 34
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson P.C.
;            STREET: 225 Franklin Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110-2804
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/137,953
;            FILING DATE: 03-May-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/888,429
;            FILING DATE: 07-JUL-1997
;            APPLICATION NUMBER: 08/530,950
;            FILING DATE: 19-SEP-1995
;            APPLICATION NUMBER: 08/446,083
;            FILING DATE: 19-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fasse, Peter J.
;            REGISTRATION NUMBER: 32,983
;            REFERENCE/DOCKET NUMBER: 07917/053001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617/542-5070
;            TELEFAX: 617/542-8906
;            TELEX: 299354
;  INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 399 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-137-953-10
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  Query Match           53.5%;  Score 888.5;  DB 16;  Length 399;
  Best Local Similarity  52.6%;  Pred. No. 1.2e-75;
  Matches  172;  Conservative   60;  Mismatches   76;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              ||||  :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         63 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 122

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || |||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db        123 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 182

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|::: 
Db        183 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALNHLKENLKIIHRDIKPSNILLDRS 240

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              |::|:|||||||| ||||:||| ||||:||||||||:|  :::||:|:|||||||||: |:
Db        241 GNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVWSLGITLYEL 300

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||        ||| |::|   || |: ::|  | |
Db        301 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEERFSPSFINFVNLCLTKDESKRPKYKE 360

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        361 LLKHPFILMYEERAVEVACYVCKILDQ 387


RESULT 14
US-09-761-569-8
; Sequence 8, Application US/09761569
; Patent No. US20020102691A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Raingeaud, Joel
;                   Gupta, Shashi
;                   Derijard, Benoit
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
;                            ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
;                            KINASES
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/761,569
;             FILING DATE: 16-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/057,009
;             FILING DATE: 1998-04-07
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, J. Peter
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/010001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 393 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: No. US20020102691A1 Relevant
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-761-569-8

  Query Match           52.6%;  Score 872.5;  DB 10;  Length 393;
  Best Local Similarity  52.3%;  Pred. No. 4e-74;
  Matches  171;  Conservative   59;  Mismatches   78;  Indels   19;  Gaps    5;

Qy          7 PNPTPPRN----------LDSRTFITIG-DRMFEVEADDLVTISELGRGAYGVVEKVRHA 55
              ||||  :|          ::|   : |  :: ::  |:||  : |:|||||| | |: |
Db         57 PNPTGVQNPHIERLRTHSIESSGKLKISPEQHWDFTAEDLKDLGEIGRGAYGSVNKMVHK 116

Qy         56 QSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMD 115
               || |||||||:||: :|||:||||||: ||: || | | |||||||||| |||||||
Db        117 PSGQIMAVKRIRSTVDEKEQKQLLMDLDVVMRSSDCPYIVQFYGALFREGDCWICMELMS 176

Qy        116 TSLDKFYR---KVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKE 172
              || ||||:    |||    |||:|||:| :: |:|| ||    | :||||:||||:|::: 
Db        177 TSFDKFYKYVYSVLDD--VIPEEILGKITLATVKALMHLKENLKIIHRDIKPSNILLDRS 234

Qy        173 GHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEM 232
              | :|:|||||| ||||:||| ||||:||||||||:   :::||:|:|||||||||: |:
Db        235 GMIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDFSASRQGYDVRSDVWSLGITLYEL 294

Qy        233 AILRFPYESWGTPFQQLKQVVEEPSPQLPAD---RFSPEFVDFTAQCLRKNPAERMSYLE 289
              |  ||||  | : | || |||:   |||        ||| |::|   || |: ::|  | |
Db        295 ATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEEREFSPSFINFVNLCLTKDESKRPKYKE 354

Qy        290 LMEHPFFTLHKTKKTDIAAFVKKILGE 316
              |::|||  ::: :  ::| :| ||| :
Db        355 LLKHPFILMYEERAVEVACYVCKILDQ 381


RESULT 15
US-10-137-953-21
; Sequence 21, Application US/10137953
; Publication No. US20030129606A1
;   GENERAL INFORMATION:
;        APPLICANT: Davis, Roger J.
;                   Whitmarsh, Alan
;                   Tournier, Cathy
;        TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
;                            ACTIVATED HUMAN PROTEIN KINASE KINASES
;        NUMBER OF SEQUENCES: 34
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/137,953
;             FILING DATE: 03-May-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/888,429
;             FILING DATE: 07-JUL-1997
;             APPLICATION NUMBER: 08/530,950
;             FILING DATE: 19-SEP-1995
;             APPLICATION NUMBER: 08/446,083
;             FILING DATE: 19-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fasse, Peter J.
;             REGISTRATION NUMBER: 32,983
;             REFERENCE/DOCKET NUMBER: 07917/053001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
```

```
;             TELEFAX: 617/542-8906
;             TELEX: 299354
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 393 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-137-953-21

  Query Match             42.0%;  Score 697;  DB 16;  Length 393;
  Best Local Similarity   45.4%;  Pred. No. 1.6e-57;
  Matches  143;  Conservative   53;  Mismatches   99;  Indels   20;  Gaps    5;

Qy          7 PNPTPPRNLDSRT----------FITIGDRMFEVEADDLVTISELGRGAYGVVEKVRH 54
              | ||||    | |              : |  | :  : :||  : :|| |  | | |: |
Db         60 PLPTPPHPPVSETDMKLKIIMEQTGKLNINGRQYPTDINDLKHLGDLGNGTSGNVVKMMH 119

Qy         55 AQSGTIMAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELM 114
                | ||:|||::| | |::| ||:|||||: ::: || | |   |   |: |||||||||
Db        120 LSSNTIIAVKQMRRTGNAEENKRILMDLDVVLKSHDCKYIVKCLGCFVRDPDVWICMELM 179

Qy        115 DTSLDKFYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGH 174
              ||  :  | |   :|| |||:: |: | || :|  |  ||||||||||:||:: |:
Db        180 SMCFDKLLK--LSKK-PVPEQILGKVTVATVNALSYLKDKHGVIHRDVKPSNILIDERGN 236

Qy        175 VKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAI 234
              :|:|||||| |||| |||  |||  |||||||:|:  :  |::::|||||||::|:|
Db        237 IKLCDFGISGRLVDSKAKTRSAGCAAYMAPERIDPK--KPKYDIRADVWSLGITLVELAT 294

Qy        235 LRFPYESWGTPFQQLKQVVEEPSPQLP---ADRFSPEFVDFTAQCLRKNPAERMSYLELM 291
               | |||   | |: | :|::   | ||      || :| ||  :|| ||  :|  | ||:
Db        295 ARSPYEGCNTDFEVLTKVLDSEPPCLPYGEGYNFSQQFRDFVIKCLTKNHQDRPKYPELL 354

Qy        292 EHPFFTLHKTKKTDI 306
              ||  :::: | |:
Db        355 AQPFIRIYESAKVDV 369


Search completed: November  5, 2003, 20:10:56
Job time : 43 secs
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RESULT 2
S71631
mitogen-activated protein kinase kinase (EC 2.7.1.-) 6 [similarity] - human
N;Alternate names: MAP kinase kinase SAPKK3
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 08-Sep-2000
C;Accession: S71631; A59347
R;Cuenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.R.
EMBO J. 15, 4156-4164, 1996
A;Title: Purification and cDNA cloning of SAPKK3, the major activator of RK/p38 in stres
A;Reference number: S71631; MUID:97015116; PMID:8861944
A;Accession: S71631
A;Molecule type: mRNA
A;Residues: 1-334 <CUE>
A;Cross-references: EMBL:X96757; NID:g1495484; PIDN:CAA65532.1; PID:g1495485
A;Experimental source: cell type B cell; cell line BJAB
R;Han, J.; Lee, J.D.; Jiang, Y.; Li, Z.; Feng, L.; Ulevitch, R.J.
J. Biol. Chem. 271, 2886-2891, 1996
A;Title: Characterization of the structure and function of a novel MAP kinase kinase (MK
A;Reference number: A59347; MUID:96216353; PMID:8621675
A;Accession: A59347
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 57-124,'M',126-334 <HAN>
A;Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671
C;Genetics:
A;Gene: GDB:MAP2K6; PRKMK6; MEK6; MKK6; SAPKK3
A;Cross-references: GDB:1230470; OMIM:601254
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;51-314/Domain: protein kinase homology <KIN>
F;59-67/Region: protein kinase ATP-binding motif

Query Match 81.9%; Score 1359; DB 2; Length 334;
Best Local Similarity 82.4%; Pred. No. 8.3e-62;
Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

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Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIMELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||:|||||| :||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
              |||||||||||||||||:|| |||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGT 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334
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RESULT 3
S71632
MAP kinase kinase (EC 2.7.1.-) SAPKK3 isoform A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
C;Accession: S71632
R;Cuenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.R.
EMBO J. 15, 4156-4164, 1996
A;Title: Purification and cDNA cloning of SAPKK3, the major activator of RK/p38 in stres
A;Reference number: S71631; MUID:97015116; PMID:8861944
A;Accession: S71632
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-334 <CUE>
A;Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A;Experimental source: cell type fibroblast
C;Genetics:
A;Gene: SAPKK3
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;51-314/Domain: protein kinase homology <KIN>
F;59-67/Region: protein kinase ATP-binding motif

Query Match 81.1%; Score 1347; DB 2; Length 334;
Best Local Similarity 81.1%; Pred. No. 3.3e-61;
Matches 253; Conservative 33; Mismatches 26; Indels 0; Gaps 0;

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Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              |  : ||||:|||:  |:||:: |||:||||  | ||||||||||:||  || |||||
Db         23 PQTSSTPPRDLDSKACISIGNQNFEVKADDLEPIVELGRGAYGVVEKMRHVPSGQIMAVK 82

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
              ||||||||||||||||||::|||||| :||||||||||||||||||||||||||::
Db         83 RIRATVNSQEQKRLLMDLDVSMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQ 142

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
              |:||  ||||||||:||||||:||||||||||||||||||||  | ||||||||||
Db        143 VIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINTLGQVKMCDFGISG 202

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
              |||||||||:|||||||||||||||||||||:||||:|||||||||:|||||||:||||
Db        203 YLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGT 262

Qy        245 PFQQLKQVVEEPSPQLPADKFSADFVDFTSQCLKKNSKERPTYPELMQHPFFTVHESKAA 304
              |||||||||||||||||:|| :|||||:|||:||  || :| |||:|||||||::| |
Db        263 PFQQLKQVVEEPSPQLPADKFSADFVDFTSQCLKKNSKERPTYPELMQHPFFTVHESKAA 322

Qy        305 DIAAFVKKILGE 316
              |:|:||| |||:
Db        323 DVASFVKLILGD 334
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RESULT 4
I38901
JNK-activating protein kinase (EC 2.7.1.-) - human
N;Alternate names: dual specificity kinase JNKK; MAP kinase kinase MKK4
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 18-Jun-1999
C;Accession: I38901; B55556
R;Lin, A.; Minden, A.; Martinetto, H.; Claret, F.X.; Lange-Carter, C.; Mercurio, F.; Joh
Science 268, 286-290, 1995
A;Title: Identification of a dual specificity kinase that activates the Jun kinases and
A;Reference number: A56160; MUID:95232504; PMID:7716521
A;Accession: I38901
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-399 <RES>
A;Cross-references: EMBL:U17743; NID:g791187; PIDN:AAC50127.1; PID:g791188
A;Note: it is uncertain whether Met-1 or Met-37 is the initiator
R;Derijard, B.; Raingeaud, J.; Barrett, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, R
Science 267, 682-685, 1995
A;Title: Independent human MAP kinase signal transduction pathways defined by MEK and MI
A;Reference number: A55556; MUID:95141073; PMID:7839144
A;Accession: B55556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 37-399 <EER>
A;Cross-references: GB:L36870
C;Genetics:
A;Gene: JNKK1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:02:42 ; Search time 18 Seconds
(without alignments)
1698.980 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1653	99.6	318	2	A55556	mitogen-activated
2	1359	81.9	334	2	S71631	mitogen-activated
3	1347	81.1	334	2	S71632	MAP kinase kinase
4	888.5	53.5	399	2	I38901	JNK-activating pro
5	882	53.1	445	2	S36039	MAP kinase activat
6	880	53.0	457	2	A54694	MAP kinase activat
7	847	51.0	395	2	S52423	protein kinase (EC
8	830.5	50.0	343	2	T16665	hypothetical prote
9	748	45.1	162	2	S71633	MAP kinase kinase
10	613	36.9	505	2	T16583	hypothetical prote
11	602.5	36.3	363	2	T22107	hypothetical prote
12	598	36.0	605	2	S18648	protein kinase wis
13	593	35.7	359	2	T26025	hypothetical prote
14	582.5	35.1	1218	2	T29915	hypothetical prote
15	573	34.5	393	1	A45100	mitogen-activated
16	573	34.5	393	1	JN0840	mitogen-activated
17	573	34.5	393	1	I59571	mitogen-activated
18	572	34.5	393	1	S42068	mitogen-activated
19	570.5	34.4	668	2	S56909	polymyxin B resist
20	569.5	34.3	401	1	I52829	mitogen-activated
21	565	34.0	400	1	A46723	MAP kinase kinase
22	564	34.0	400	1	A48081	mitogen-activated
23	563	33.9	393	1	S46361	mitogen-activated
24	563	33.9	395	1	S36186	mitogen-activated
25	550	33.1	397	1	S41054	mitogen-activated
26	545.5	32.9	393	2	A45176	protein kinase Dso
27	521	31.4	355	2	T02056	protein kinase MEK
28	510.5	30.8	444	2	A56708	MAPK/ERK kinase 5
29	506	30.5	435	2	T37324	probable JNK-activ
30	500	30.1	387	1	A56466	mitogen-activated
31	489	29.5	354	2	T04262	mitogen-activated
32	488.5	29.4	448	2	T16256	hypothetical prote
33	476.5	28.7	357	2	T06583	protein kinase MEK
34	467.5	28.2	363	2	T08542	mitogen-activated
35	466.5	28.1	363	2	T51735	mitogen-activated
36	466	28.1	363	2	T51992	MAP kinase kinase
37	462	27.8	363	2	T51294	MAP kinase kinase
38	452	27.2	506	2	S69045	protein kinase MKK
39	452	27.2	508	2	A48069	protein kinase MKK
40	450.5	27.1	518	2	S53804	protein kinase NPK
41	447	26.9	515	2	A25048	regulatory protein
42	433.5	26.1	340	1	OKBYR1	protein kinase byr
43	418.5	25.2	520	2	T51338	mitogen-activated
44	366.5	22.1	366	2	T51339	mitogen-activated
45	365.5	22.0	449	2	T16259	hypothetical prote

ALIGNMENTS

RESULT 1
A55556
mitogen-activated protein kinase kinase (EC 2.7.1.-) 3 [similarity] - human
N;Alternate names: MAP kinase kinase 3 (MKK3)
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Sep-2000
C;Accession: A55556
R;Derijard, B.; Raingeaud, J.; Barrett, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, R
Science 267, 682-685, 1995
A;Title: Independent human MAP kinase signal transduction pathways defined by MEK and M
A;Reference number: A55556; MUID:95141073; PMID:7839144
A;Accession: A55556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-318 <EER>
A;Cross-references: GB:L36719; NID:g685173; PIDN:AAC41718.1; PID:g685174
C;Genetics:
A;Gene: GDB:MAP2K3; PRKMK3; MEK3; MKK3
A;Cross-references: GDB:9539640; OMIM:602315
A;Map position: 17q11.2-17q11.2
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;33-296/Domain: protein kinase homology <KIN>
F;41-49/Region: protein kinase ATP-binding motif

Query Match 99.6%; Score 1653; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.4e-76;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||||||||||
Db        301 TKKTDIAAFVKKILGEDS 318
```

```
                  |||||||:||||||||||||:||||||||||||||||||||||||||||||||||||||||::
Db        153 RIRATVNTQEQKRLLMDLDISMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYKQ 212

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
                  | :| |||||||||:| ||||:||||||| ||||||||||||||| :| ||||||||||
Db        213 VHEKGMTIPEDILGKITVSIVKALEHLHSNLSVIHRDVKPSNVLINMQGQVKMCDFGISG 272

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
                  |||||||||||||||||||||||| |||||||||:|||||||||:|||||||:||||
Db        273 YLVDSVAKTMDAGCKPYMAPERINPETNQKGYNVKSDIWSLGITMIELAILRFPYDSWGT 332

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
                  |||||||||||||||||||||||||||:||||||  || :| |||:||||||:| :| |
Db        333 PFQQLKQVVEEPSPQLPADRFSPEFVDFTSQCLRKNSKERPTYTELMQHPFFTIHDSKDT 392

Qy        305 DIAAFVKKILGE 316
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Db        393 DVASFVKSILGD 404


RESULT 2
Q9DGE0
ID   Q9DGE0      PRELIMINARY;      PRT;   363 AA.
AC   Q9DGE0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   MKK3.
GN   MAP2K3 OR ZMKK3.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20451058; PubMed=10995439;
RA   Fujii R., Yamashita S., Hibi M., Hirano T.;
RT   "Asymmetric p38 Activation in Zebrafish: Its Possible Role in
RT   Symmetric and Synchronous Cleavage.";
RL   J. Cell Biol. 150:1335-1348(2000).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AB030899; BAB11809.1; -.
DR   ZFIN; ZDB-GENE-010202-3; map2k3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   363 AA;  40807 MW;  02A7CD9A6F5A2D2C CRC64;

  Query Match           83.5%;  Score 1386;  DB 13;  Length 363;
  Best Local Similarity   82.7%;  Pred. No. 1.1e-114;
  Matches  258;  Conservative   28;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
                  ||| |||||:|||: ::|||:: | |:|||  | ||||||||||:|:||  || |||||
Db         52 PAPAPTPPRDLDSKAYVTIGEKNFVVKADDLEQIGELGRGAYGVVDKMRHVPSGVIMAVK 111

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
                  |||||||:|||||||||||:||||||||||||||||||||||||||||||||||||::
Db        112 RIRATVNTQEQKRLLMDLDISMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYKQ 171

Qy        125 VLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISG 184
                  | :|  ||||||||:| ||||:||||||| ||||||||||||||| :| ||||||||||
Db        172 VHEKGKTIPEDILGKITVSIVKALEHLHSNLSVIHRDVKPSNVLINMQGQVKMCDFGISG 231

Qy        185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGT 244
                  |||||||||||||||||||||||| |||||||||:|||||||||:|||||||:||||
Db        232 YLVDSVAKTMDAGCKPYMAPERINPETNQKGYNVKSDIWSLGITMIELAILRFPYDSWGT 291

Qy        245 PFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTKKT 304
                  |||||||||||||||||||||||| :|||||:|||||  || :| |||:||||||:| :| |
Db        292 PFQQLKQVVEEPSPQLPADRFSADFVDFTSQCLRKNSTERPTYTELMQHPFFTLHDSKDT 351

Qy        305 DIAAFVKKILGE 316
                  |:|:||| |||:
Db        352 DVASFVKTILGD 363


RESULT 3
Q9PW48
ID   Q9PW48      PRELIMINARY;      PRT;   335 AA.
AC   Q9PW48;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   MAP kinase activator XMEK3.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065138; PubMed=10597270;
RA   Kieran M.W., Katz S., Vail B., Zon L.I., Mayer B.J.;
RT   "Concentration-dependent positive and negative regulation of a MAP
RT   kinase by a MAP kinase kinase.";
RL   Oncogene 18:6647-6657(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Keiran M., Vail B., Zon L.I., Mayer B.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AF172848; AAD49421.1; -.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   335 AA;  37923 MW;  29369A6D25B4DB57 CRC64;

  Query Match           82.6%;  Score 1371;  DB 13;  Length 335;
  Best Local Similarity   81.8%;  Pred. No. 2e-113;
  Matches  257;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 KPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMA 62
                  :|   :|||||:|||:  | ||:: |||:|||  | ||||||||||:||   |  |||
Db         22 QPQVSSPTPPRDLDSKACILIGEKNFEVKADDLEPIEELGRGAYGVVEKMRHVPSEQIMA 81

Qy         63 VKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFY 122
                  |||||||||||||||||||||:|||||| :|||||||||||||||||||||||||||||
Db         82 VKRIRATVNSQEQKRLLMDLDISMRTVDCHFTVTFYGALFREGDVWICMELMDTSLDKFY 141

Qy        123 RKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGI 182
                  : |:|| :|||||||:||||||:|||||||||||||||||||||||||| ||||||||
Db        142 KNVIDKGLTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINKEGQVKMCDFGI 201

Qy        183 SGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESW 242
                  |||||||||||||||||||||||||||||||||||:||||:|||||||||||||||:||
Db        202 SGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIEMAILRFPYDSW 261

Qy        243 GTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHKTK 302
                  |||||||||||||||||:|| ||||||::||:||   | :| |||:|||| ||::
Db        262 GTPFQQLKQVVEEPSPQLPADKFSAEFVDFTSKCLKKNSKGRPTYSELMQHPFFVLHESM 321

Qy        303 KTDIAAFVKKILGE 316
                  ||:|:|||:|||:
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:02:02 ; Search time 28 Seconds
(without alignments)
2930.740 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1395	84.0	404	13	Q9I959	Q9i959 cyprinus ca
2	1386	83.5	363	13	Q9DGE0	Q9dge0 brachydanio
3	1371	82.6	335	13	Q9PW48	Q9pw48 xenopus lae
4	1346	81.1	334	11	Q925D6	Q925d6 rattus norv
5	1343	80.9	334	11	Q8BP44	Q8bp44 mus musculu
6	1199	72.2	293	11	Q8C371	Q8c371 mus musculu
7	1162	70.0	301	11	Q8BPT2	Q8bpt2 mus musculu
8	1078	64.9	237	11	Q60521	Q60521 mus musculu
9	1044	62.9	335	5	Q9U983	Q9u983 drosophila
10	1038	62.5	334	5	O62602	O62602 drosophila
11	891.5	53.7	407	13	Q8UW90	Q8uw90 cyprinus ca
12	835.5	50.3	336	5	Q95YI9	Q95yi9 caenorhabdi
13	823	49.6	424	5	O61444	O61444 drosophila
14	816	49.2	281	11	Q8K2U0	Q8k2u0 mus musculu
15	816	49.2	281	13	Q9DGR7	Q9dgr7 brachydanio
16	748	45.1	162	11	P70273	P70273 mus musculu
17	694	41.8	492	5	O18411	O18411 drosophila
18	694	41.8	1178	5	Q8SZZ1	Q8szz1 drosophila
19	665	40.1	419	11	Q8BSP1	Q8bsp1 mus musculu
20	664	40.0	389	11	O35720	O35720 mus musculu
21	664	40.0	391	11	O35872	O35872 mus musculu
22	664	40.0	419	11	O35871	O35871 mus musculu
23	664	40.0	435	11	Q9R1Z5	Q9r1z5 mus musculu
24	664	40.0	468	11	O54780	O54780 mus musculu
25	664	40.0	535	11	Q8CE90	Q8ce90 mus musculu
26	661	39.8	346	11	Q9QWG6	Q9qwg6 mus musculu
27	660.5	39.8	453	11	Q9R1Z4	Q9r1z4 mus musculu
28	660.5	39.8	469	11	Q9R1Z6	Q9r1z6 mus musculu
29	657.5	39.6	380	11	Q9R1Z3	Q9r1z3 mus musculu
30	656.5	39.5	426	4	Q8IY10	Q8iy10 homo sapien
31	655	39.5	346	11	O35406	O35406 mus musculu
32	650.5	39.2	356	5	Q95UF5	Q95uf5 ancylostoma
33	644	38.8	417	13	Q8QHK7	Q8qhk7 xenopus lae
34	606	36.5	347	5	Q21307	Q21307 caenorhabdi
35	593	35.7	359	5	O01706	O01706 caenorhabdi
36	583	35.1	371	5	Q23326	Q23326 caenorhabdi
37	583	35.1	411	5	Q8MPS3	Q8mps3 caenorhabdi
38	573	34.5	393	11	Q9JJE1	Q9jje1 mus musculu
39	571	34.4	400	11	Q91YS7	Q91ys7 mus musculu
40	570.5	34.4	401	11	Q9D7B0	Q9d7b0 mus musculu
41	563	33.9	393	6	Q9XT09	Q9xt09 pan troglod
42	559.5	33.7	683	3	Q96W50	Q96w50 debaryomyce
43	555	33.4	439	11	Q8K360	Q8k360 mus musculu
44	551.5	33.2	448	11	Q9WVS7	Q9wvs7 mus musculu
45	547.5	33.0	448	4	Q92961	Q92961 homo sapien

ALIGNMENTS

RESULT 1
Q9I959
ID Q9I959 PRELIMINARY; PRT; 404 AA.
AC Q9I959;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAP kinase kinase 6 (MKK6).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto H.;
RT "p38 MAPK cascade in fish.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB023480; BAA96414.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 404 AA; 45370 MW; 698435FF24057059 CRC64;

Query Match 84.0%; Score 1395; DB 13; Length 404;
Best Local Similarity 83.3%; Pred. No. 2e-115;
Matches 260; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

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Qy          5 PAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVK 64
              | | |||||:|||:  :||||: | |:||||  | ||||||||||:|:||  || |||||
Db         93 PQPAPTPPRDLDSKACVTIGDKNFVVKADDLEQIGELGRGAYGVVDKMRHVPSGVIMAVK 152

Qy         65 RIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRK 124
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RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   MUTAGENESIS OF SER-218 AND THR-222.
RX   MEDLINE=96182129; PubMed=8622669;
RA   Raingeaud J., Whitmarsh A.J., Barrett T., Derijard B., Davis R.J.;
RT   "MKK3- and MKK6-regulated gene expression is mediated by the p38
RT   mitogen-activated protein kinase signal transduction pathway.";
RL   Mol. Cell. Biol. 16:1247-1255(1996).
RN   [6]
RP   VARIANTS COLON CANCER TRP-175 AND VAL-215.
RX   MEDLINE=21309069; PubMed=11414763;
RA   Teng D.-H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.C.;
RT   "Mutation analyses of 268 candidate genes in human tumor cell lines.";
RL   Genomics 74:352-364(2001).
CC   -!- FUNCTION: Dual specificity kinase. Is activated by cytokines and
CC       environmental stress in vivo. Catalyzes the concomitant
CC       phosphorylation of a threonine and a tyrosine residue in the MAP
CC       kinase p38.
CC   -!- ENZYME REGULATION: Activated by dual phosphorylation on Ser-218
CC       and Thr-222.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=3; Synonyms=3b;
CC         IsoId=P46734-1; Sequence=Displayed;
CC       Name=1;
CC         IsoId=P46734-2; Sequence=VSP_004878;
CC       Name=2; Synonyms=3c;
CC         IsoId=P46734-3; Sequence=VSP_004877;
CC   -!- TISSUE SPECIFICITY: Abundant expression is seen in the skeletal
CC       muscle. It is also widely expressed in other tissues.
CC   -!- PTM: Autophosphorylated.
CC   -!- DISEASE: Defects in MAP2K3 may be involved in colon cancer.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP
CC       KINASE KINASE SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L36719; AAC41718.1; -.
DR   EMBL; D87116; BAA13248.1; -.
DR   EMBL; U66839; AAB40652.1; -.
DR   EMBL; U66840; AAB40653.1; -.
DR   EMBL; BC032478; AAH32478.1; -.
DR   Genew; HGNC:6843; MAP2K3.
DR   MIM; 602315; -.
DR   GO; GO:0004708; F:MAP kinase kinase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW   ATP-binding; Phosphorylation; Alternative splicing; Disease mutation.
FT   DOMAIN       64    325       PROTEIN KINASE.
FT   NP_BIND      70     78       ATP (BY SIMILARITY).
FT   BINDING      93     93       ATP (BY SIMILARITY).
FT   ACT_SITE    190    190       BY SIMILARITY.
FT   MOD_RES     218    218       PHOSPHORYLATION.
FT   MOD_RES     222    222       PHOSPHORYLATION.
FT   VARSPLIC      1     16       MESPASSQPASMPQSK -> MGVQGTLMSRDSQTPHLLSIL
FT                                (in isoform 2).
FT                                /FTId=VSP_004877.
FT   VARSPLIC      1     29       Missing (in isoform 1).
FT                                /FTId=VSP_004878.
FT   VARIANT     175    175       R -> W (IN COLON CANCER).
FT                                /FTId=VAR_014208.
FT   VARIANT     215    215       L -> V (IN COLON CANCER).
FT                                /FTId=VAR_014209.
FT   MUTAGEN     218    218       S->E: CONSTITUTIVE ACTIVATION.
FT   MUTAGEN     218    218       S->A: INACTIVATION.
FT   MUTAGEN     222    222       T->E: CONSTITUTIVE ACTIVATION.
FT   MUTAGEN     222    222       T->A: INACTIVATION.
FT   CONFLICT    341    341       E -> K (IN REF. 1 AND 3).
SQ   SEQUENCE   347 AA;  39318 MW;  A80BA4FDFF8F75A2 CRC64;

  Query Match             99.3%;  Score 1649;  DB 1;  Length 347;
  Best Local Similarity   99.4%;  Pred. No. 6e-116;
  Matches  316;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSKPPAPNPTPPRNLDSRTFITIGDRMFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         30 MSKPPAPNPTPPRNLDSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTI 89

Qy         61 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 MAVKRIRATVNSQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDK 149

Qy        121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDF 209

Qy        181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYE 269

Qy        241 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 SWGTPFQQLKQVVEEPSPQLPADRFSPEFVDFTAQCLRKNPAERMSYLELMEHPFFTLHK 329

Qy        301 TKKTDIAAFVKKILGEDS 318
              ||||||||||:||||||
Db        330 TKKTDIAAFVKEILGEDS 347


RESULT 2
MPK3_MOUSE
ID   MPK3_MOUSE     STANDARD;      PRT;   347 AA.
AC   O09110; P97293; Q91VX1;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Dual specificity mitogen-activated protein kinase kinase 3
DE   (EC 2.7.1.-) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERK kinase 3).
GN   MAP2K3 OR PRKMK3 OR MKK3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Neininger A., Gaestel M.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=97059154; PubMed=8900184;
RA   Moriguchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,
RA   Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;
RT   "Purification and identification of a major activator for p38 from
RT   osmotically shocked cells. Activation of mitogen-activated protein
RT   kinase kinase 6 by osmotic shock, tumor necrosis factor-alpha, and
RT   H2O2.";
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2003, 20:00:51 ; Search time 11 Seconds
(without alignments)
1359.499 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPTPPRNLDSRTF.....HKTKKTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1649	99.3	347	1	MPK3_HUMAN	P46734 homo sapien
2	1613	97.2	347	1	MPK3_MOUSE	O09110 mus musculu
3	1359	81.9	334	1	MPK6_HUMAN	P52564 homo sapien
4	1347	81.1	334	1	MPK6_MOUSE	P70236 mus musculu
5	888.5	53.5	399	1	MPK4_HUMAN	P45985 homo sapien
6	882	53.1	446	1	MPK2_XENLA	Q07192 xenopus lae
7	881	53.1	397	1	MPK4_MOUSE	P47809 m dual spec
8	697	42.0	487	1	HEP_DROME	Q23977 drosophila
9	670	40.4	419	1	MPK7_HUMAN	O14733 homo sapien
10	602.5	36.3	363	1	YR62_CAEEL	Q20347 caenorhabdi
11	598	36.0	605	1	WIS1_SCHPO	P33886 schizosacch
12	573	34.5	392	1	MPK1_HUMAN	Q02750 homo sapien
13	573	34.5	392	1	MPK1_MOUSE	P31938 mus musculu
14	573	34.5	392	1	MPK1_RAT	Q01986 rattus norv
15	572	34.5	392	1	MPK1_RABIT	P29678 oryctolagus
16	570.5	34.4	668	1	PBS2_YEAST	P08018 saccharomyc
17	569.5	34.3	401	1	MPK2_MOUSE	Q63932 mus musculu
18	569	34.3	388	1	MPK1_SERCA	Q91447 serinus can
19	565	34.0	400	1	MPK2_HUMAN	P36507 homo sapien
20	564	34.0	400	1	MPK2_RAT	P36506 rattus norv
21	563	33.9	393	1	MPK1_CRIGR	Q63980 cricetulus
22	563	33.9	394	1	MPK1_XENLA	Q05116 xenopus lae
23	563	33.9	398	1	MPK2_CHICK	Q90891 gallus gall
24	550.5	33.2	448	1	MPK5_RAT	Q62862 rattus norv
25	550	33.1	397	1	MPK2_CYPCA	Q90321 cyprinus ca
26	545.5	32.9	393	1	DSOR_DROME	Q24324 drosophila
27	517.5	31.2	438	1	MPK5_HUMAN	Q13163 homo sapien
28	500	30.1	387	1	MEK2_CAEEL	Q10664 caenorhabdi
29	489.5	29.5	435	1	FUZ7_USTMA	Q99078 ustilago ma
30	462	27.8	363	1	SKH1_SCHPO	Q9y884 schizosacch
31	452	27.2	506	1	MKK2_YEAST	P32491 saccharomyc
32	452	27.2	508	1	MKK1_YEAST	P32490 saccharomyc
33	447	26.9	515	1	STE7_YEAST	P06784 saccharomyc
34	445	26.8	491	1	STK3_HUMAN	Q13188 homo sapien
35	433.5	26.1	340	1	BYR1_SCHPO	P10506 schizosacch
36	431.5	26.0	487	1	STK4_HUMAN	Q13043 homo sapien
37	370	22.3	968	1	STKA_HUMAN	O94804 homo sapien
38	359	21.6	966	1	STKA_MOUSE	O55098 mus musculu
39	358	21.6	916	1	TNIK_MOUSE	P83510 mus musculu
40	358	21.6	1360	1	TNIK_HUMAN	Q9uke5 homo sapien
41	350	21.1	1332	1	M4K6_HUMAN	Q8n4c8 homo sapien
42	347	20.9	1308	1	M4K6_MOUSE	Q9jm52 mus musculu
43	346	20.8	471	1	SID1_SCHPO	O14305 schizosacch
44	346	20.8	1239	1	M4K4_HUMAN	O95819 homo sapien
45	333	20.1	894	1	M4K3_HUMAN	Q8ivh8 homo sapien

ALIGNMENTS

RESULT 1
MPK3_HUMAN
ID MPK3_HUMAN STANDARD; PRT; 347 AA.
AC P46734; Q99441; Q9UE71; Q9UE72;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dual specificity mitogen-activated protein kinase kinase 3
DE (EC 2.7.1.-) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERK kinase 3).
GN MAP2K3 OR PRKMK3 OR MKK3 OR MEK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95141073; PubMed=7839144;
RA Derijard B., Raingeaud J., Barrett T., Wu I.-H., Han J.,
RA Ulevitch R.J., Davis R.J.;
RT "Independent human MAP-kinase signal transduction pathways defined by
RT MEK and MKK isoforms.";
RL Science 267:682-685(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=97059154; PubMed=8900184;
RA Moriguchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,
RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;
RT "Purification and identification of a major activator for p38 from
RT osmotically shocked cells: Activation of mitogen-activated protein
RT kinase kinase 6 by osmotic shock, tumor necrosis factor-alpha, and
RT H2O2.";
RL J. Biol. Chem. 271:26981-26988(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RA Han J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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Set     Items   Description
S1        227   AU='DAVIS ROGER J'
S2         16   S1 AND MKK3
S3         12   RD S2 (unique items)
S4          9   ANTIBOD?(10N)(MKK3)
S5          6   RD S4 (unique items)
S6       1304   ANTIBOD?(20N)(MITOGEN(W)ACTIVATED(W)PROTEIN(W)KINASE?)
S7        700   S6 AND (ANTIBOD?)(30N)(TREAT? OR THERAP? OR INHIBIT? OR SU-
           PPRESS? OR MODULAT? OR PREVENT?)
S8         47   S7 AND REVIEW?
S9         46   RD S8 (unique items)
S10        29   S7 AND (KINASE? OR MKK?)(20N)(DISEASE? OR DISORDER?)
S11        24   RD S10 (unique items)
S12        54   MKK? (20N)(DISEASE? OR DISORDER?)
S13        31   RD S12 (unique items)
S14       626   MKK3
S15       116   MKK3 AND (DISEASE? OR DISORDER?)
S16        76   RD S15 (unique items)
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